SEQUENCE LISTING

<110> MARINE BIOTECHNOLOGY INSTITUTE CO., LTD.

<120> METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING GYRASE GENE AS AN INDICATOR

<130> PH-581

<140> US09/208,688

<141> 1998-12-10

<150> JP97/343316

<151> 1997-12-12

<160> 80

<170> PatentIn version 2.0

<210> 1

<211> 1212

<212> DNA

<213> Bacteroides vulgatus

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<221> CDS

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tct tgt gtg aac gcc ttg tct act cac atg acc aca cag gta ttc cgc 96
Ser Cys Val Asn Ala Leu Ser Thr His Met Thr Thr Gln Val Phe Arg
20 25 30
ggt ggc aag atc tac cag cag gaa tac agc tgc gga cat cct ttg tat 144
Gly Gly Lys Ile Tyr Gln Gln Glu Tyr Ser Cys Gly His Pro Leu Tyr
35 40 45
tct gta aaa gaa gta gga aca gct gat att acc gga aca aaa cag act 192
Ser Val Lys Glu Val Gly Thr Ala Asp Ile Thr Gly Thr Lys Gln Thr
50 55 60
ttc tgg ccg gat gat acc atc ttc act gtt acc gaa tat aag ttt gac 240
Phe Trp Pro Asp Asp Thr Ile Phe Thr Val Thr Glu Tyr Lys Phe Asp
65 70 75 80
att cta cag gca cgt atg cgt gaa ttg gcc tac ttg aac aaa ggt atc 288
Ile Leu Gln Ala Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly Ile
85 90 95
acc att tca ctg acc gac cgc cgg atc aaa gaa gaa gat ggc agc ttc 336
Thr Ile Ser Leu Thr Asp Arg Arg Ile Lys Glu Glu Asp Gly Ser Phe
100 105 110
aag aaa gaa ata ttc cat tcg gac gaa gga gtg aaa gag ttt gta cgt 384
Lys Lys Glu Ile Phe His Ser Asp Glu Gly Val Lys Glu Phe Val Arg
115 120 125
ttc ctg aac cgt aac aac gaa gcg ctg att aat gat gtc att tat ctg 432
Phe Leu Asn Arg Asn Asn Glu Ala Leu Ile Asn Asp Val Ile Tyr Leu
130 135 140
aat acc gaa aaa aac aat acc ccc att gaa tgt gcc atc atg tac aat 480
Asn Thr Glu Lys Asn Asn Thr Pro Ile Glu Cys Ala Ile Met Tyr Asn

145 150 155 160

aca ggc tat cgt gaa agc ctg cat tcg tat gta aac aat atc aat aca 528

Thr Gly Tyr Arg Glu Ser Leu His Ser Tyr Val Asn Asn Ile Asn Thr

165 170 175

ata gaa ggc ggt aca cac gag gcc ggt ttc cgc agc gca tta acc cgt 576

Ile Glu Gly Gly Thr His Glu Ala Gly Phe Arg Ser Ala Leu Thr Arg

180 185 190

gta ctg aag aaa tat gcg gaa gat acc aaa gca ctg gaa aaa gca aaa 624

Val Leu Lys Lys Tyr Ala Glu Asp Thr Lys Ala Leu Glu Lys Ala Lys

195 200 205

gtc gag att tcg gga gag gac ttc cgc gaa ggc ttg att gcc gtc att 672

Val Glu Ile Ser Gly Glu Asp Phe Arg Glu Gly Leu Ile Ala Val Ile

210 215 220

tca gtg aaa gta gcc gag ccg cag ttc gaa gga cag acc aag acc aag 720

Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys

225 230 235 240

ctg ggc aac agc gaa gtg agt ggt gcc gtg aac caa gct gta ggc gaa 768

Leu Gly Asn Ser Glu Val Ser Gly Ala Val Asn Gln Ala Val Gly Glu

245 250 255

gcg ctt aca tat tat ctg gaa gaa cat ccg aaa gaa gca aaa cag att 816

Ala Leu Thr Tyr Tyr Leu Glu Glu His Pro Lys Glu Ala Lys Gln Ile

260 265 270

gtt gac aaa gtg atc ctg gct gca aca gcg cgt atc gcc gca cgc aag 864

Val Asp Lys Val Ile Leu Ala Ala Thr Ala Arg Ile Ala Ala Arg Lys

275 280 285

gca cgt gaa tct gtt caa aga aag agt ccg atg ggc ggt ggc gga ctg 912

Ala Arg Glu Ser Val Gln Arg Lys Ser Pro Met Gly Gly Gly Gly Leu

290 295 300

ccg ggc aaa ctg gcc gac tgc tcg agc cgt aat ccg gag gaa tgt gaa 960

Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asn Pro Glu Glu Cys Glu
305 310 315 320

cta ttc ctg gtc gag ggt gac tcg gca ggt ggt tct gcc aag caa gga 1008
Leu Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly
325 330 335

cgt agc cgt gcc ttc cag gca att cta cct ttg agg ggt aaa atc ctg 1056
Arg Ser Arg Ala Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu
340 345 350

aat gtg gaa aaa gcg atg tgg cac aag gct ttt gaa agc gat gag gtc 1104
Asn Val Glu Lys Ala Met Trp His Lys Ala Phe Glu Ser Asp Glu Val
355 360 365

aat aat atc atc acc gcc ctg ggt gtc cgt ttc ggt gtg gac gga aat 1152
Asn Asn Ile Ile Thr Ala Leu Gly Val Arg Phe Gly Val Asp Gly Asn
370 375 380

gat gac agc aaa aaa gcg aac atc gac aag ctg cgt tat cac aaa gtg 1200
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Val Ile Met Thr

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<213> Bacteroides vulgatus

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Gly Gly Lys Ile Tyr Gln Gln Glu Tyr Ser Cys Gly His Pro Leu Tyr

35 40 45

Ser Val Lys Glu Val Gly Thr Ala Asp Ile Thr Gly Thr Lys Gln Thr

50 55 60

Phe Trp Pro Asp Asp Thr Ile Phe Thr Val Thr Glu Tyr Lys Phe Asp

65 70 75 80

Ile Leu Gln Ala Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly Ile

85 90 95

Thr Ile Ser Leu Thr Asp Arg Arg Ile Lys Glu Glu Asp Gly Ser Phe

100 105 110

Lys Lys Glu Ile Phe His Ser Asp Glu Gly Val Lys Glu Phe Val Arg

115 120 125

Phe Leu Asn Arg Asn Asn Glu Ala Leu Ile Asn Asp Val Ile Tyr Leu

130 135 140

Asn Thr Glu Lys Asn Asn Thr Pro Ile Glu Cys Ala Ile Met Tyr Asn

145 150 155 160

Thr Gly Tyr Arg Glu Ser Leu His Ser Tyr Val Asn Asn Ile Asn Thr

165 170 175

Ile Glu Gly Gly Thr His Glu Ala Gly Phe Arg Ser Ala Leu Thr Arg

180 185 190

Val Leu Lys Lys Tyr Ala Glu Asp Thr Lys Ala Leu Glu Lys Ala Lys

195 200 205

Val Glu Ile Ser Gly Glu Asp Phe Arg Glu Gly Leu Ile Ala Val Ile

210 215 220

Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys

225 230 235 240

Leu Gly Asn Ser Glu Val Ser Gly Ala Val Asn Gln Ala Val Gly Glu

245 250 255

Ala Leu Thr Tyr Tyr Leu Glu Glu His Pro Lys Glu Ala Lys Gln Ile
260 265 270
Val Asp Lys Val Ile Leu Ala Ala Thr Ala Arg Ile Ala Ala Arg Lys
275 280 285
Ala Arg Glu Ser Val Gln Arg Lys Ser Pro Met Gly Gly Gly Gly Leu
290 295 300
Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asn Pro Glu Glu Cys Glu
305 310 315 320
Leu Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly
325 330 335
Arg Ser Arg Ala Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu
340 345 350
Asn Val Glu Lys Ala Met Trp His Lys Ala Phe Glu Ser Asp Glu Val
355 360 365
Asn Asn Ile Ile Thr Ala Leu Gly Val Arg Phe Gly Val Asp Gly Asn
370 375 380
Asp Asp Ser Lys Lys Ala Asn Ile Asp Lys Leu Arg Tyr His Lys Val
385 390 395 400
Val Ile Met Thr

<210> 3
<211> 1263
<212> DNA
<213> Mycobacterium simiae

<220>
<221> CDS
<222> (1)... (1263)

<400> 3

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Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
 1               5                  10                  15

gtg tcg gtg gtc aac gcc ctg tcc acc cgc ctg gaa gtc aac gtc aag    96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Val Lys
            20                  25                  30

cgt gac ggc tat gag tgg ttc cag tac tac gac cgg gcg gtg ccc ggc   144
Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
        35                  40                  45

acc ctc aag caa ggc gag gcg acc aag aag acc ggc acc acg atc cgg   192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
    50                  55                  60

ttc tgg gcc gat cct gag atc ttc gaa acc acc cag tac gac ttc gag   240
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65                  70                  75                  80

acg gtg gcg cgc cgg ttg cag gaa atg gcg ttc ctc aac aag ggc ctg   288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                85                  90                  95

acc atc aac ctc acc gac gaa cgt gtc gag cag gac gag gtg gtc gat   336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
            100                 105                 110

gag gtg gtt agc gac acc gcc gag gcg ccg aag tca gcc gag gag cag   384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln
        115                 120                 125

gcg gcc gaa tcg gcc aag ccg cac aag gtc aag cac cgc acg ttc cac   432
Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

tac ccg ggt ggg ttg gtg gat ttc gtc aag cac atc aat cgc acc aaa   480
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Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys

145 150 155 160

aac ccg atc cag cag agc gtc atc gac ttc gac ggc aaa gga acc ggg 528

Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly

165 170 175

cac gaa gtc gag atc gcg atg cag tgg aac ggt ggt tat tcg gag tcg 576

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser

180 185 190

gtg cac acc ttc gcc aac acc atc aac acc cat gag ggc ggc acc cac 624

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His

195 200 205

gag gag ggc ttc cgc agc gcg ctg acc tcg gtg gtg aac aag tac gcc 672

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala

210 215 220

aaa gac aag aag ctg ctc aag gac aag gat ccc aac ctc acc ggc gac 720

Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp

225 230 235 240

gac atc cga gaa ggg ctg gcc gcg gtg atc tcc gtg aag gtc gcc gag 768

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu

245 250 255

ccg cag ttc gag ggc cag act aag acg aaa ctc ggc aac acc gag gtc 816

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val

260 265 270

aag tcg ttt gtc cag aaa gtc tgt aac gaa caa ctc act cac tgg ttc 864

Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe

275 280 285

gag gcg aac ccg tcg gaa gct aaa acc gtt gta aac aag gcg gtt tcg 912

Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser

290 295 300

tcg gcc cag gcc cgc att gcg gcg cgt aag gcg cgg gag ttg gtg cgg 960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305 310 315 320

cgt aag agt gct acg gat ttg ggt ggg ttg ccg ggc aag ttg gct gat 1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
325 330 335

tgc cgc tcg acg gat ccg cgg aag tct gag ctg tat gtg gtg gaa ggt 1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
340 345 350

gat tcc gcg ggt ggg tcg gcg aaa agt ggg cgt gat tcg atg ttc cag 1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
355 360 365

gcg atc ttg ccg ctg cgc ggc aag atc atc aac gtc gaa aag gcc cgc 1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
370 375 380

atc gat cgg gtg ctg aaa aac acc gaa gtc cag gcc atc atc acc gcg 1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385 390 395 400

ctg ggc acc ggc atc cac gac gaa ttc gac atc acc aaa ctg cgt tac 1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
405 410 415

cac aag atc gtg ttg 1263
His Lys Ile Val Leu
420

<210> 4

<211> 421

<212> PRT

<213> Mycobacterium simiae

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            20   25   30

Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
        35   40   45

Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
    50   55   60

Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65   70   75   80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                85   90   95

Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
            100   105   110

Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln
        115   120   125

Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His
    130   135   140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145   150   155   160

Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
                165   170   175

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180   185   190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195   200   205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala

210 215 220

Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp

225 230 235 240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu

245 250 255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val

260 265 270

Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe

275 280 285

Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser

290 295 300

Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg

305 310 315 320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp

325 330 335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly

340 345 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln

355 360 365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg

370 375 380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala

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405 410 415

His Lys Ile Val Leu

420

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<211> 660

<212> DNA

<213> Chitinophaga pinensis

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<221> CDS

<222> (1)... (660)

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 1               5                  10                  15

gat aag aac aaa atg ttc gaa aaa acc aag atc gaa gta aca ggt gat    96
Asp Lys Asn Lys Met Phe Glu Lys Thr Lys Ile Glu Val Thr Gly Asp
            20                  25                  30

gac ttc cgt gaa ggt ctg agc gct atc atc agc gta aaa gta cct gaa   144
Asp Phe Arg Glu Gly Leu Ser Ala Ile Ile Ser Val Lys Val Pro Glu
        35                  40                  45

cca cag ttc gaa ggc cag acc aaa acc aaa ctc ggt aac tcc gat gta   192
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Ser Asp Val
    50                  55                  60

atg ggg gtt gtg gac agt tcc gta gca gcc gta ctg gat gcc tac ctg   240
Met Gly Val Val Asp Ser Ser Val Ala Ala Val Leu Asp Ala Tyr Leu
65                  70                  75                  80

gaa gaa cat ccc cgc gaa gcc aag atc att atc aat aaa gtg gta ctg   288
Glu Glu His Pro Arg Glu Ala Lys Ile Ile Ile Asn Lys Val Val Leu
                85                  90                  95

gca gca cag gcg cgt gaa gca gcc cgt aaa gca cgc cag atg gta cag   336
Ala Ala Gln Ala Arg Glu Ala Ala Arg Lys Ala Arg Gln Met Val Gln
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100 105 110

cgt aag agc gta ctg agt gga agc ggc ttg cct ggt aaa ctg gct gac 384

Arg Lys Ser Val Leu Ser Gly Ser Gly Leu Pro Gly Lys Leu Ala Asp

115 120 125

tgc tct gaa aat gat cct gaa aaa tgt gaa ctg tac ctg gta gag ggt 432

Cys Ser Glu Asn Asp Pro Glu Lys Cys Glu Leu Tyr Leu Val Glu Gly

130 135 140

gac tcc gca ggt ggt acg gct aaa caa gga cgt aac cgt agc ttc cag 480

Asp Ser Ala Gly Gly Thr Ala Lys Gln Gly Arg Asn Arg Ser Phe Gln

145 150 155 160

gcg atc ctg ccg ctc agg ggt aaa atc ctg aac gtg gag aaa gcc atg 528

Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Met

165 170 175

gag cat aag ata tat gag aat gag gag att aaa aac atc ttc acc gca 576

Glu His Lys Ile Tyr Glu Asn Glu Glu Ile Lys Asn Ile Phe Thr Ala

180 185 190

ctt ggt gta acc atc ggt acg gaa gaa gat gac aaa gcc ctc aac ctc 624

Leu Gly Val Thr Ile Gly Thr Glu Glu Asp Asp Lys Ala Leu Asn Leu

195 200 205

tcc aaa ctg cgc tat cac aaa ctg atc atc atg acg 660

Ser Lys Leu Arg Tyr His Lys Leu Ile Ile Met Thr

210 215 220

<210> 6

<211> 220

<212> PRT

<213> Chitinophaga pinensis

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            20   25   30

Asp Phe Arg Glu Gly Leu Ser Ala Ile Ile Ser Val Lys Val Pro Glu

        35   40   45

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Ser Asp Val

    50   55   60

Met Gly Val Val Asp Ser Ser Val Ala Ala Val Leu Asp Ala Tyr Leu

65   70   75   80

Glu Glu His Pro Arg Glu Ala Lys Ile Ile Ile Asn Lys Val Val Leu

                85   90   95

Ala Ala Gln Ala Arg Glu Ala Ala Arg Lys Ala Arg Gln Met Val Gln

            100   105   110

Arg Lys Ser Val Leu Ser Gly Ser Gly Leu Pro Gly Lys Leu Ala Asp

        115   120   125

Cys Ser Glu Asn Asp Pro Glu Lys Cys Glu Leu Tyr Leu Val Glu Gly

    130   135   140

Asp Ser Ala Gly Gly Thr Ala Lys Gln Gly Arg Asn Arg Ser Phe Gln

145   150   155   160

Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Met

                165   170   175

Glu His Lys Ile Tyr Glu Asn Glu Glu Ile Lys Asn Ile Phe Thr Ala

            180   185   190

Leu Gly Val Thr Ile Gly Thr Glu Glu Asp Asp Lys Ala Leu Asn Leu

        195   200   205

Ser Lys Leu Arg Tyr His Lys Leu Ile Ile Met Thr

    210   215   220

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<211> 537

<212> DNA

<213> Flavobacterium aquatile

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<221> CDS

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Ser Cys Val Asn Ala Leu Ser Asp Asn Leu Lys Ala Thr Val Phe Arg
20 25 30

gac gga aaa gtg tac gag caa gaa tat gaa aaa ggt aaa gca atg tat 144
Asp Gly Lys Val Tyr Glu Gln Glu Tyr Glu Lys Gly Lys Ala Met Tyr
35 40 45

ccg gtt aag caa gtt ggt gaa aca aca aag cga gga aca atg gtt act 192
Pro Val Lys Gln Val Gly Glu Thr Thr Lys Arg Gly Thr Met Val Thr
50 55 60

ttt cat cct gat aaa acc att ttt act caa aca att gag tat tct tat 240
Phe His Pro Asp Lys Thr Ile Phe Thr Gln Thr Ile Glu Tyr Ser Tyr
65 70 75 80

gat aca ctt gca gca cgt atg cgt gaa tta tct ttc ctg aat aaa gga 288
Asp Thr Leu Ala Ala Arg Met Arg Glu Leu Ser Phe Leu Asn Lys Gly
85 90 95

att aca atc aca ctt aca gat aaa aga cat act aaa gac aac ggc gat 336

Ile Thr Ile Thr Leu Thr Asp Lys Arg His Thr Lys Asp Asn Gly Asp
100 105 110

ttt gaa ggt gaa gtt ttt cat tct aaa gaa ggg ctt aaa gaa ttc gtt 384
Phe Glu Gly Glu Val Phe His Ser Lys Glu Gly Leu Lys Glu Phe Val
115 120 125

cga ttt tta gat gct ggt aga gaa cca att att tct cac gta ata agc 432
Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser
130 135 140

atg gag cac gaa aaa gga gaa gtt cct gtt gag gtt gct ctt gtt tac 480
Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr
145 150 155 160

aat aca agt tac tcc gaa aat att ttc tct tac gta aat aat att aac 528
Asn Thr Ser Tyr Ser Glu Asn Ile Phe Ser Tyr Val Asn Asn Ile Asn
165 170 175

acg cac gaa 537
Thr His Glu

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<212> PRT
<213> Flavobacterium aquatile

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Asp Gly Lys Val Tyr Glu Gln Glu Tyr Glu Lys Gly Lys Ala Met Tyr
35 40 45

Pro Val Lys Gln Val Gly Glu Thr Thr Lys Arg Gly Thr Met Val Thr
50 55 60

Phe His Pro Asp Lys Thr Ile Phe Thr Gln Thr Ile Glu Tyr Ser Tyr
65 70 75 80

Asp Thr Leu Ala Ala Arg Met Arg Glu Leu Ser Phe Leu Asn Lys Gly
85 90 95

Ile Thr Ile Thr Leu Thr Asp Lys Arg His Thr Lys Asp Asn Gly Asp
100 105 110

Phe Glu Gly Glu Val Phe His Ser Lys Glu Gly Leu Lys Glu Phe Val
115 120 125

Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser
130 135 140

Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr
145 150 155 160

Asn Thr Ser Tyr Ser Glu Asn Ile Phe Ser Tyr Val Asn Asn Ile Asn
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Thr His Glu

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<211> 783

<212> DNA

<213> Mycobacterium asiaticum

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<221> CDS

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1 5 10 15

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Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys
20 25 30

cgc gac ggg cac gag tgg ttt cag tac tac gac cgc gcc gtg ccc gga 144
Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
35 40 45

acc ctc aag cag ggc gag gcc acc aag aag acc gga acc acg atc agg 192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60

ttc tgg gcg gac ccc gaa atc ttc gaa acc aca cag tac gac ttc gag 240
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65 70 75 80

acc gtg gcg cgg cgg ctg cag gag atg gcc ttc ctc aac aag ggc ctc 288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95

acc atc aac ctc acc gac gaa cga gtg gag cag gac gag gtc gtc gac 336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
100 105 110

gag gtc gtc agc gac acc gcc gag gca ccg aag tcc gcc gaa gag aag 384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
115 120 125

gcc gcg gaa tcg act gcg cca cac aag gtc aag cac cgc acc ttc cac 432
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
130 135 140

tac ccc ggc ggt ctg gtc gac ttc gtc aag cac atc aac cgc acc aag 480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys

145 150 155 160

agc ccg atc cag cag agc gtc atc gat ttc gac ggc aag ggc acc ggc 528

Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly

165 170 175

cac gag gtc gag atc gcc atg cag tgg aac ggc ggc tac tcg gag tcc 576

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser

180 185 190

gtc cac acc ttc gcc aac acc atc aac acg cac gag ggc ggc acc cac 624

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His

195 200 205

gag gag ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc 672

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala

210 215 220

aaa gac aag aaa ctg ctg aag gac aaa gat ccc aac ctc acc ggt gac 720

Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp

225 230 235 240

gac atc cgt gag ggc ttg gcc gcg gtc atc tcg gtg aag gtc gcc gag 768

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu

245 250 255

cca cag ttc gaa ggc 783

Pro Gln Phe Glu Gly

260

<210> 10

<211> 261

<212> PRT

<213> Mycobacterium asiaticum

<400> 10

Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys
20 25 30
Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
35 40 45
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65 70 75 80
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
100 105 110
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
115 120 125
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
130 135 140
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145 150 155 160
Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
165 170 175
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
180 185 190
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
195 200 205
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
210 215 220
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp

225 230 235 240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu

245 250 255

Pro Gln Phe Glu Gly

260

<210> 11

<211> 195

<212> DNA

<213> Cytophaga lytica

<220>

<221> CDS

<222> (1)... (195)

<400> 11

agc cac att gaa act tta att ctt aca ttc ttc ttc cgt ttt atg cga 48

Ser His Ile Glu Thr Leu Ile Leu Thr Phe Phe Phe Arg Phe Met Arg

1 5 10 15

gaa cta ata gaa ggc gga cac gtt tac ata gca aca cca cct tta tat 96

Glu Leu Ile Glu Gly Gly His Val Tyr Ile Ala Thr Pro Pro Leu Tyr

20 25 30

tta gtt aaa aaa gga act aaa aag cgt tat gct tgg aat gat aaa gaa 144

Leu Val Lys Lys Gly Thr Lys Lys Arg Tyr Ala Trp Asn Asp Lys Glu

35 40 45

cga gat gaa ata gca gat agc ttt aat ggt agt gta ggt atc caa aga 192

Arg Asp Glu Ile Ala Asp Ser Phe Asn Gly Ser Val Gly Ile Gln Arg

50 55 60

tat 195

Tyr

65

<210> 12

<211> 65

<212> PRT

<213> Cytophaga lytica

<400> 12

Ser His Ile Glu Thr Leu Ile Leu Thr Phe Phe Phe Arg Phe Met Arg

1 5 10 15

Glu Leu Ile Glu Gly Gly His Val Tyr Ile Ala Thr Pro Pro Leu Tyr

20 25 30

Leu Val Lys Lys Gly Thr Lys Lys Arg Tyr Ala Trp Asn Asp Lys Glu

35 40 45

Arg Asp Glu Ile Ala Asp Ser Phe Asn Gly Ser Val Gly Ile Gln Arg

50 55 60

Tyr

65

<210> 13

<211> 1170

<212> DNA

<213> Synechococcus sp.

<220>

<221> CDS

<222> (1)... (1170)

<400> 13

gtg gtg gac aac gcc gtc gac aaa gcc ttg gcg ggc tac tgc aat acc 48

Val Val Asp Asn Ala Val Asp Lys Ala Leu Ala Gly Tyr Cys Asn Thr

1 5 10 15

att gat gtt cgt ctg ctc aaa gac ggc tcc tgc caa gtc acc gat aac 96

Ile Asp Val Arg Leu Leu Lys Asp Gly Ser Cys Gln Val Thr Asp Asn

20 25 30

ggt cgc ggc att ccc aca gat att cac ccc caa acc ggg aag tct gct 144

Gly Arg Gly Ile Pro Thr Asp Ile His Pro Gln Thr Gly Lys Ser Ala

35 40 45

ctc gaa acc gtg ctg acg att ctg cac gcg ggc ggc aag ttt ggc ggt 192

Leu Glu Thr Val Leu Thr Ile Leu His Ala Gly Gly Lys Phe Gly Gly

50 55 60

ggc ggt tat aag gtg tcg ggg ggt ctg cac ggc gtc ggt gtg tct gtc 240

Gly Gly Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser Val

65 70 75 80

gtc aac gcc ctc tca gaa tat gtc gaa gtc acc gtg tgg cgg gaa ggc 288

Val Asn Ala Leu Ser Glu Tyr Val Glu Val Thr Val Trp Arg Glu Gly

85 90 95

aaa acc cac caa cag cgc ttt gaa cag ggc aac ccg atc ggg gag ttg 336

Lys Thr His Gln Gln Arg Phe Glu Gln Gly Asn Pro Ile Gly Glu Leu

100 105 110

caa gtt gcc ccg gat gcc gac gat cgc cgc ggg aca caa gtt cgt ttc 384

Gln Val Ala Pro Asp Ala Asp Asp Arg Arg Gly Thr Gln Val Arg Phe

115 120 125

aaa cca gac gcc acg atc ttt tct gaa aca acc gag ttc gat tac ggc 432

Lys Pro Asp Ala Thr Ile Phe Ser Glu Thr Thr Glu Phe Asp Tyr Gly

130 135 140

acc cta gca agc cga ttg aag gag cta gcc tat ctg aat gcg ggc gtc 480

Thr Leu Ala Ser Arg Leu Lys Glu Leu Ala Tyr Leu Asn Ala Gly Val
145 150 155 160

cgc atc gac ttt acc gat gag cgg ctg cag ctc acc aag aat cac gag 528
Arg Ile Asp Phe Thr Asp Glu Arg Leu Gln Leu Thr Lys Asn His Glu
165 170 175

ccc cat caa gaa acc tat tac ttt gaa ggc ggt att cgc gaa tac gtc 576
Pro His Gln Glu Thr Tyr Tyr Phe Glu Gly Gly Ile Arg Glu Tyr Val
180 185 190

gcc tac atg aat acc gat aaa cag gcg ctg cac tca gag att atc ttt 624
Ala Tyr Met Asn Thr Asp Lys Gln Ala Leu His Ser Glu Ile Ile Phe
195 200 205

gtg caa tcc gaa aaa gat ggc gtc caa gtt gaa gct gca ttg caa tgg 672
Val Gln Ser Glu Lys Asp Gly Val Gln Val Glu Ala Ala Leu Gln Trp
210 215 220

tgc gtt gac gcc tac agc gac aac att ctg ggc ttt gcc aac aac atc 720
Cys Val Asp Ala Tyr Ser Asp Asn Ile Leu Gly Phe Ala Asn Asn Ile
225 230 235 240

cgc acg att gac ggc ggc acc cat att gag ggg ctc aaa act gtt ctg 768
Arg Thr Ile Asp Gly Gly Thr His Ile Glu Gly Leu Lys Thr Val Leu
245 250 255

acg cgg acg atg aac acg atc gcc cgc aaa cgg aat aaa cgc aag gat 816
Thr Arg Thr Met Asn Thr Ile Ala Arg Lys Arg Asn Lys Arg Lys Asp
260 265 270

gcc gac aat aac ctg tcg ggc gag aat att cgc gaa ggg tta aca gcg 864
Ala Asp Asn Asn Leu Ser Gly Glu Asn Ile Arg Glu Gly Leu Thr Ala
275 280 285

atc gtt tcg gtc aaa gtt ccg gat ccg gaa ttt gaa ggg caa acc aaa 912
Ile Val Ser Val Lys Val Pro Asp Pro Glu Phe Glu Gly Gln Thr Lys
290 295 300

aca aag ctc ggc aat acc gaa gtt cgc ggc atc gtc gat acg ctc gtg 960
Thr Lys Leu Gly Asn Thr Glu Val Arg Gly Ile Val Asp Thr Leu Val
305 310 315 320
ggc gaa acg ttg acg gaa tat ctg gaa ttc cat ccc agc gtt gcc gat 1008
Gly Glu Thr Leu Thr Glu Tyr Leu Glu Phe His Pro Ser Val Ala Asp
325 330 335
ttg atc ctc gaa aaa gcg att caa gcc ttt aat gcg gct gag gca gcg 1056
Leu Ile Leu Glu Lys Ala Ile Gln Ala Phe Asn Ala Ala Glu Ala Ala
340 345 350
cga cgg gca cgg gaa ttg gtg cgt cgc aaa tca gtg ctg gaa tct tcg 1104
Arg Arg Ala Arg Glu Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser
355 360 365
aca ttg ccc ggt aaa tta gca gac tgt tcc agt cgc gat ccc ggt gaa 1152
Thr Leu Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu
370 375 380
tct gaa atc ttc atc gtg 1170
Ser Glu Ile Phe Ile Val
385 390

<210> 14
<211> 390
<212> PRT
<213> Synechoccus sp.

<400> 14
Val Val Asp Asn Ala Val Asp Lys Ala Leu Ala Gly Tyr Cys Asn Thr
1 5 10 15
Ile Asp Val Arg Leu Leu Lys Asp Gly Ser Cys Gln Val Thr Asp Asn
20 25 30

Gly Arg Gly Ile Pro Thr Asp Ile His Pro Gln Thr Gly Lys Ser Ala
35 40 45
Leu Glu Thr Val Leu Thr Ile Leu His Ala Gly Gly Lys Phe Gly Gly
50 55 60
Gly Gly Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser Val
65 70 75 80
Val Asn Ala Leu Ser Glu Tyr Val Glu Val Thr Val Trp Arg Glu Gly
85 90 95
Lys Thr His Gln Gln Arg Phe Glu Gln Gly Asn Pro Ile Gly Glu Leu
100 105 110
Gln Val Ala Pro Asp Ala Asp Asp Arg Arg Gly Thr Gln Val Arg Phe
115 120 125
Lys Pro Asp Ala Thr Ile Phe Ser Glu Thr Thr Glu Phe Asp Tyr Gly
130 135 140
Thr Leu Ala Ser Arg Leu Lys Glu Leu Ala Tyr Leu Asn Ala Gly Val
145 150 155 160
Arg Ile Asp Phe Thr Asp Glu Arg Leu Gln Leu Thr Lys Asn His Glu
165 170 175
Pro His Gln Glu Thr Tyr Tyr Phe Glu Gly Gly Ile Arg Glu Tyr Val
180 185 190
Ala Tyr Met Asn Thr Asp Lys Gln Ala Leu His Ser Glu Ile Ile Phe
195 200 205
Val Gln Ser Glu Lys Asp Gly Val Gln Val Glu Ala Ala Leu Gln Trp
210 215 220
Cys Val Asp Ala Tyr Ser Asp Asn Ile Leu Gly Phe Ala Asn Asn Ile
225 230 235 240
Arg Thr Ile Asp Gly Gly Thr His Ile Glu Gly Leu Lys Thr Val Leu
245 250 255
Thr Arg Thr Met Asn Thr Ile Ala Arg Lys Arg Asn Lys Arg Lys Asp

260 265 270

Ala Asp Asn Asn Leu Ser Gly Glu Asn Ile Arg Glu Gly Leu Thr Ala

275 280 285

Ile Val Ser Val Lys Val Pro Asp Pro Glu Phe Glu Gly Gln Thr Lys

290 295 300

Thr Lys Leu Gly Asn Thr Glu Val Arg Gly Ile Val Asp Thr Leu Val

305 310 315 320

Gly Glu Thr Leu Thr Glu Tyr Leu Glu Phe His Pro Ser Val Ala Asp

325 330 335

Leu Ile Leu Glu Lys Ala Ile Gln Ala Phe Asn Ala Ala Glu Ala Ala

340 345 350

Arg Arg Ala Arg Glu Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser

355 360 365

Thr Leu Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu

370 375 380

Ser Glu Ile Phe Ile Val

385 390

<210> 15

<211> 696

<212> DNA

<213> Caulobacter crescentus

<220>

<221> CDS

<222> (1)... (696)

<400> 15

cag aac agc tac aag gtc tcg ggc ggt ctg cac ggc gtg ggc gtc tcg 48

Gln Asn Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser

1 5 10 15

gtc gtg aac gcc ctg tcg gat tgg ctg gag ctg ctg atc cac cgc aac 96

Val Val Asn Ala Leu Ser Asp Trp Leu Glu Leu Leu Ile His Arg Asn

20 25 30

ggc aag gtc cac cag atg cgc ttc gag cgc ggc gac gcg gtc acc tcg 144

Gly Lys Val His Gln Met Arg Phe Glu Arg Gly Asp Ala Val Thr Ser

35 40 45

ctg aag gtc acc ggc gac tcg ccc gtg cgg acc gag ggc ccc aag gcc 192

Leu Lys Val Thr Gly Asp Ser Pro Val Arg Thr Glu Gly Pro Lys Ala

50 55 60

ggc gag acc ctg acc ggt acg gaa gtt acg ttc ttt ccg tcg aag gac 240

Gly Glu Thr Leu Thr Gly Thr Glu Val Thr Phe Phe Pro Ser Lys Asp

65 70 75 80

acc ttc gcc ttc atc gaa ttc gac cgg aag acg ctg gag cac cgc ctg 288

Thr Phe Ala Phe Ile Glu Phe Asp Arg Lys Thr Leu Glu His Arg Leu

85 90 95

cgc gag ctg gcc ttc ctg aac tcg ggc gtg acg atc tgg ttc aag gac 336

Arg Glu Leu Ala Phe Leu Asn Ser Gly Val Thr Ile Trp Phe Lys Asp

100 105 110

cat cgc gac gtc gag ccg tgg gaa gag aag ctg ttc tac gag ggc ggc 384

His Arg Asp Val Glu Pro Trp Glu Glu Lys Leu Phe Tyr Glu Gly Gly

115 120 125

atc gag gcc ttc gtg cgc cac ctc gac aag gcc aag acg ccg ctg ctg 432

Ile Glu Ala Phe Val Arg His Leu Asp Lys Ala Lys Thr Pro Leu Leu

130 135 140

aag gcc ccg atc gcc gtc aag ggc gtc aag gac aag gtc gag atc gac 480

Lys Ala Pro Ile Ala Val Lys Gly Val Lys Asp Lys Val Glu Ile Asp

145 150 155 160

ctg gcc ctg tgg tgg aac gac agc tac cac gag cag atg ctg tgc ttc 528
Leu Ala Leu Trp Trp Asn Asp Ser Tyr His Glu Gln Met Leu Cys Phe
165 170 175

acc aac aac atc ccg cag cgg gat ggc ggc acg cac ctg tcg gcc ttt 576
Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ser Ala Phe
180 185 190

cgc gcg gcc ctg acc cgg atc atc acc agc tac gcc gag agc tcc ggc 624
Arg Ala Ala Leu Thr Arg Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly
195 200 205

atc ctg aag aag gaa aag gtc agc ctg ggc ggc gaa gac agc cgc gag 672
Ile Leu Lys Lys Glu Lys Val Ser Leu Gly Gly Glu Asp Ser Arg Glu
210 215 220

ggc ctg acc tgc gtg ctg tcg gtc 696
Gly Leu Thr Cys Val Leu Ser Val
225 230

<210> 16
<211> 232
<212> PRT
<213> Caulobacter crescentus

<400> 16
Gln Asn Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser
1 5 10 15

Val Val Asn Ala Leu Ser Asp Trp Leu Glu Leu Leu Ile His Arg Asn
20 25 30

Gly Lys Val His Gln Met Arg Phe Glu Arg Gly Asp Ala Val Thr Ser
35 40 45

Leu Lys Val Thr Gly Asp Ser Pro Val Arg Thr Glu Gly Pro Lys Ala

50 55 60

Gly Glu Thr Leu Thr Gly Thr Glu Val Thr Phe Phe Pro Ser Lys Asp

65 70 75 80

Thr Phe Ala Phe Ile Glu Phe Asp Arg Lys Thr Leu Glu His Arg Leu

85 90 95

Arg Glu Leu Ala Phe Leu Asn Ser Gly Val Thr Ile Trp Phe Lys Asp

100 105 110

His Arg Asp Val Glu Pro Trp Glu Glu Lys Leu Phe Tyr Glu Gly Gly

115 120 125

Ile Glu Ala Phe Val Arg His Leu Asp Lys Ala Lys Thr Pro Leu Leu

130 135 140

Lys Ala Pro Ile Ala Val Lys Gly Val Lys Asp Lys Val Glu Ile Asp

145 150 155 160

Leu Ala Leu Trp Trp Asn Asp Ser Tyr His Glu Gln Met Leu Cys Phe

165 170 175

Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ser Ala Phe

180 185 190

Arg Ala Ala Leu Thr Arg Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly

195 200 205

Ile Leu Lys Lys Glu Lys Val Ser Leu Gly Gly Glu Asp Ser Arg Glu

210 215 220

Gly Leu Thr Cys Val Leu Ser Val

225 230

<210> 17

<211> 888

<212> DNA

<213> Pseudomonas putida

<220>

<221> CDS

<222> (1)... (888)

<400> 17

ggc ggc ctg cac ggt gta ggc gtg tcg gta gtg aac gca ctg tct gaa 48

Gly Gly Leu His Gly Val Gly Val Ser Val Val Asn Ala Leu Ser Glu

1 5 10 15

gag ctc gtc ctc acc gtt cgc cgt agc ggc aag atc tgg gaa cag acc 96

Glu Leu Val Leu Thr Val Arg Arg Ser Gly Lys Ile Trp Glu Gln Thr

20 25 30

tac gtc cat ggt gtt ccg cag gaa ccg atg aag atc gtt ggc gac agc 144

Tyr Val His Gly Val Pro Gln Glu Pro Met Lys Ile Val Gly Asp Ser

35 40 45

gaa acc acc ggc acc cag atc cac ttc aag gct tcc agc gaa acc ttc 192

Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe

50 55 60

aag aac atc cac ttc agc tgg gac atc ctg gcc aag cgg att cgt gaa 240

Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu

65 70 75 80

ctg tcc ttc ctc aac tcc ggt gtc ggc atc gtc ctc aag gat gag cgc 288

Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg

85 90 95

agc ggc aag gaa gaa ctg ttc aag tac gaa ggc ggc ttg cgc gcg ttc 336

Ser Gly Lys Glu Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe

100 105 110

gtt gaa tac ctg aac acc aac aag acc ccg gtc aac cag gtg ttc cat 384

Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His

115 120 125

ttc aac atc cag cgc gaa gac ggc atc ggc gta gaa atc gcc ctg cag 432
Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln
130 135 140

tgg aac gac agc ttc aac gag aac ctg ttg tgc ttc acc aac aac att 480
Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile
145 150 155 160

ccg cag cgc gat ggc ggt act cac ctg gtg ggt ttc cgt tcc gcc ctg 528
Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu
165 170 175

acg cgt aac ctc aat acg tat atc gaa gcc gaa ggc ctg gcg aag aag 576
Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys
180 185 190

cac aag gtc gcg acc acc ggt gac gat gcc cgt gaa ggc ctg gcc gcg 624
His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala
195 200 205

atc att tcg gta aaa gtg ccg gat ccg aag ttc agc tcc cag acc aag 672
Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys
210 215 220

gac aag ctg gtt tct tcc gaa gtg aag acc gcg gtc gaa cag gaa atg 720
Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met
225 230 235 240

ggc aag tac ttc tcc gac ttc ctg ctg gaa aac ccg aac gaa gcc aag 768
Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys
245 250 255

ctg gtt gtc ggc aag atg atc gac gcg gca cgt gct cgt gaa gcg gcg 816
Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala
260 265 270

cgc aag acc cgt gag atg acc cgc cgc aaa ggc gcg ctg gac atc gcc 864
Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala

275 280 285

ggc ctg ccg ggc aaa ctg gct gac 888

Gly Leu Pro Gly Lys Leu Ala Asp

290 295

<210> 18

<211> 296

<212> PRT

<213> Pseudomonas putida

<400> 18

Gly Gly Leu His Gly Val Gly Val Ser Val Val Asn Ala Leu Ser Glu

1 5 10 15

Glu Leu Val Leu Thr Val Arg Arg Ser Gly Lys Ile Trp Glu Gln Thr

20 25 30

Tyr Val His Gly Val Pro Gln Glu Pro Met Lys Ile Val Gly Asp Ser

35 40 45

Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe

50 55 60

Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu

65 70 75 80

Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg

85 90 95

Ser Gly Lys Glu Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe

100 105 110

Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His

115 120 125

Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln

130 135 140

Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile
145 150 155 160
Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu
165 170 175
Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys
180 185 190
His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala
195 200 205
Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys
210 215 220
Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met
225 230 235 240
Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys
245 250 255
Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala
260 265 270
Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala
275 280 285
Gly Leu Pro Gly Lys Leu Ala Asp
290 295

<210> 19
<211> 531
<212> DNA
<213> Synechococcus sp.

<220>
<221> CDS
<222> (1)... (531)

<400> 19

ttg gtg cgt cgc aaa tca gtg ctg gaa tct tcg aca ttg ccc ggt aaa 48
Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser Thr Leu Pro Gly Lys
1 5 10 15

tta gca gac tgt tcc agt cgc gat ccc ggt gaa tct gaa atc ttc atc 96
Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu Ser Glu Ile Phe Ile
20 25 30

gtg gaa ggg gat tcg gca ggt ggc agt gct aaa cag ggg cgc gat cgc 144
Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly Arg Asp Arg
35 40 45

cgc ttc caa gcc atc ctg cct ctg cgc ggc aaa atc ctc aac atc gag 192
Arg Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Ile Glu
50 55 60

aaa acg gac gat gcc aaa atc tac aaa aac act gag atc caa gcc ctg 240
Lys Thr Asp Asp Ala Lys Ile Tyr Lys Asn Thr Glu Ile Gln Ala Leu
65 70 75 80

att aca gcg ctg ggc ctc gga att aaa ggg gag gaa ttt gat gct tcc 288
Ile Thr Ala Leu Gly Leu Gly Ile Lys Gly Glu Glu Phe Asp Ala Ser
85 90 95

caa ctg cgc tac cac cgt att gtg atc atg act gac gcg gac gtc gat 336
Gln Leu Arg Tyr His Arg Ile Val Ile Met Thr Asp Ala Asp Val Asp
100 105 110

ggt gcg cac atc cgt acc ctc ttg ctc acc ttc ttc tat cgc tat cag 384
Gly Ala His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr Arg Tyr Gln
115 120 125

cga tcg ctg ctg gag cag ggc tac atg tac att gcc tgc ccg ccg ctg 432
Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu
130 135 140

tac aag ttg gag cgg gga cgt aat cac tac tat tgc tac aac gaa cgc 480
Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg
145 150 155 160
gaa ctg cag gaa cgg att gcg acg ttc cct gaa aac gcc aac tat acg 528
Glu Leu Gln Glu Arg Ile Ala Thr Phe Pro Glu Asn Ala Asn Tyr Thr
165 170 175
att 531
Ile

<210> 20
<211> 177
<212> PRT
<213> Synechococcus sp.

<400> 20
Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser Thr Leu Pro Gly Lys
1 5 10 15
Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu Ser Glu Ile Phe Ile
20 25 30
Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly Arg Asp Arg
35 40 45
Arg Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Ile Glu
50 55 60
Lys Thr Asp Asp Ala Lys Ile Tyr Lys Asn Thr Glu Ile Gln Ala Leu
65 70 75 80
Ile Thr Ala Leu Gly Leu Gly Ile Lys Gly Glu Glu Phe Asp Ala Ser
85 90 95
Gln Leu Arg Tyr His Arg Ile Val Ile Met Thr Asp Ala Asp Val Asp
100 105 110

Gly Ala His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr Arg Tyr Gln
115 120 125
Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu
130 135 140
Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg
145 150 155 160
Glu Leu Gln Glu Arg Ile Ala Thr Phe Pro Glu Asn Ala Asn Tyr Thr
165 170 175
Ile

<210> 21
<211> 660
<212> DNA
<213> Caulobacter crescentus

<220>
<221> CDS
<222> (1)... (660)

<400> 21
cgg gat ggc ggc acg cac ctg tcg gcc ttt cgc gcg gcc ctg acc cgg 48
Arg Asp Gly Gly Thr His Leu Ser Ala Phe Arg Ala Ala Leu Thr Arg
1 5 10 15
atc atc acc agc tac gcc gag agc tcc ggc atc ctg aag aag gaa aag 96
Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly Ile Leu Lys Lys Glu Lys
20 25 30
gtc agc ctg ggc ggc gaa gac agc cgc gag ggc ctg acc tgc gtg ctg 144
Val Ser Leu Gly Gly Glu Asp Ser Arg Glu Gly Leu Thr Cys Val Leu
35 40 45

tcg gtc aag gtc ccg gat ccg aag ttc agc tcg cag acc aag gac aag 192
Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys Asp Lys
50 55 60

ctg gtc tcg tcc gaa gtg cgc ccc gcc gtt gag ggc ctg gtg tcg gaa 240
Leu Val Ser Ser Glu Val Arg Pro Ala Val Glu Gly Leu Val Ser Glu
65 70 75 80

ggt ctc tcg acc tgg ttc gag gaa cat ccg aac gag gcc aag gcg atc 288
Gly Leu Ser Thr Trp Phe Glu Glu His Pro Asn Glu Ala Lys Ala Ile
85 90 95

gtg acc aag atc gcc gag gcc gcc gcc gcc cgc gag gcc gcc cgc aag 336
Val Thr Lys Ile Ala Glu Ala Ala Ala Ala Arg Glu Ala Ala Arg Lys
100 105 110

gcg cga gag ctg acc cgc cgc aag agc gcg ctc gac atc acc agc ctg 384
Ala Arg Glu Leu Thr Arg Arg Lys Ser Ala Leu Asp Ile Thr Ser Leu
115 120 125

ccc ggc aag ctc gcc gac tgc tcg gaa cgc gat ccg gcc aag tcc gag 432
Pro Gly Lys Leu Ala Asp Cys Ser Glu Arg Asp Pro Ala Lys Ser Glu
130 135 140

atc ttc atc gtc gag ggc gac tcg gcg ggc ggc tcg gcc aag cag gcc 480
Ile Phe Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Ala
145 150 155 160

cgc aac cgc gac aac cag gcc gtt ctg ccc ctg cgc ggc aag atc ctg 528
Arg Asn Arg Asp Asn Gln Ala Val Leu Pro Leu Arg Gly Lys Ile Leu
165 170 175

aac gtc gag cgg gcc cgc ttc gac aag atg ctg tcg tcc gac cag atc 576
Asn Val Glu Arg Ala Arg Phe Asp Lys Met Leu Ser Ser Asp Gln Ile
180 185 190

ggc acg ctg atc acc gcc ctg ggc gcg ggg atc ggc cgc gac gac ttc 624
Gly Thr Leu Ile Thr Ala Leu Gly Ala Gly Ile Gly Arg Asp Asp Phe

195 200 205

aac ccg gac aag gtg cgc tac cac aag atc gtg ctg 660

Asn Pro Asp Lys Val Arg Tyr His Lys Ile Val Leu

210 215 220

<210> 22

<211> 220

<212> PRT

<213> Caulobacter crescentus

<400> 22

Arg Asp Gly Gly Thr His Leu Ser Ala Phe Arg Ala Ala Leu Thr Arg

1 5 10 15

Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly Ile Leu Lys Lys Glu Lys

20 25 30

Val Ser Leu Gly Gly Glu Asp Ser Arg Glu Gly Leu Thr Cys Val Leu

35 40 45

Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys Asp Lys

50 55 60

Leu Val Ser Ser Glu Val Arg Pro Ala Val Glu Gly Leu Val Ser Glu

65 70 75 80

Gly Leu Ser Thr Trp Phe Glu Glu His Pro Asn Glu Ala Lys Ala Ile

85 90 95

Val Thr Lys Ile Ala Glu Ala Ala Ala Ala Arg Glu Ala Ala Arg Lys

100 105 110

Ala Arg Glu Leu Thr Arg Arg Lys Ser Ala Leu Asp Ile Thr Ser Leu

115 120 125

Pro Gly Lys Leu Ala Asp Cys Ser Glu Arg Asp Pro Ala Lys Ser Glu

130 135 140

Ile Phe Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Ala
145 150 155 160
Arg Asn Arg Asp Asn Gln Ala Val Leu Pro Leu Arg Gly Lys Ile Leu
165 170 175
Asn Val Glu Arg Ala Arg Phe Asp Lys Met Leu Ser Ser Asp Gln Ile
180 185 190
Gly Thr Leu Ile Thr Ala Leu Gly Ala Gly Ile Gly Arg Asp Asp Phe
195 200 205
Asn Pro Asp Lys Val Arg Tyr His Lys Ile Val Leu
210 215 220

<210> 23
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<212> DNA
<213> Cytophaga lytica

<220>
<221> CDS
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<400> 23
gat aaa gat tca tac aaa gta tct ggt ggt tta cac ggt gta ggt gta 48
Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val
1 5 10 15
tct tgt gta aac gca tta tct aat aat tta aaa gct act gtt tac aga 96
Ser Cys Val Asn Ala Leu Ser Asn Asn Leu Lys Ala Thr Val Tyr Arg
20 25 30
gaa ggt aaa ata tgg gag caa gag tat gaa aga ggt aag gct tta tat 144
Glu Gly Lys Ile Trp Glu Gln Glu Tyr Glu Arg Gly Lys Ala Leu Tyr

35 40 45

ccg gta aaa agt att gga gaa aca gag gaa aca ggt act ata gtt act 192
Pro Val Lys Ser Ile Gly Glu Thr Glu Glu Thr Gly Thr Ile Val Thr
50 55 60

ttt tac cca gat gat act ata ttt aca caa act aca gag tat aat tat 240
Phe Tyr Pro Asp Asp Thr Ile Phe Thr Gln Thr Thr Glu Tyr Asn Tyr
65 70 75 80

gaa acg ctt tct aac aga atg cga gag ttg gct tac ctt aat aag gga 288
Glu Thr Leu Ser Asn Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly
85 90 95

gtt aca att agc att aca gat aag aga gtt aaa gat gaa aag gga gag 336
Val Thr Ile Ser Ile Thr Asp Lys Arg Val Lys Asp Glu Lys Gly Glu
100 105 110

ttt tta tct gaa gtt ttt tac tct gaa gaa gga cta aaa gaa ttt att 384
Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile
115 120 125

aag ttt tta gac ggt aac aga gaa caa cta ata cgt gat gtt gtt tca 432
Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser
130 135 140

atg gaa ggt gaa aaa aac gga att cct gtt gag gtt gca atg gtg tac 480
Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr
145 150 155 160

aat aca tca tat tca gaa aat ctt cac tct tac gta aat aat att aat 528
Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn
165 170 175

aca cat gaa ggt ggt aca cac ctt tca ggt ttt aga aga ggt tta aca 576
Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr
180 185 190

tca acc tta aaa aag tat gca gat gca tct gga atg tta gac aaa tta 624

Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu

195 200 205

aag ttt gag att cag gga gat gat ttt aga gaa ggt tta acg gct att 672

Lys Phe Glu Ile Gln Gly Asp Asp Phe Arg Glu Gly Leu Thr Ala Ile

210 215 220

gtg tct gtt aaa gtt gca gaa cct cag ttt gaa ggg caa aca aaa act 720

Val Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr

225 230 235 240

aaa tta ggt aac aga gaa gtt tct tct gca gtg agc caa gct gta tca 768

Lys Leu Gly Asn Arg Glu Val Ser Ser Ala Val Ser Gln Ala Val Ser

245 250 255

gaa atg ctt acc aac tat tta gaa gaa aac cca gat gat gct aag gta 816

Glu Met Leu Thr Asn Tyr Leu Glu Glu Asn Pro Asp Asp Ala Lys Val

260 265 270

att gta caa aaa gtc att ttg gca gcg caa gca cgt cat gcg gct aca 864

Ile Val Gln Lys Val Ile Leu Ala Ala Gln Ala Arg His Ala Ala Thr

275 280 285

aaa gcc cgt gaa atg gta cag cgt aaa acg gta atg agt ata ggt ggt 912

Lys Ala Arg Glu Met Val Gln Arg Lys Thr Val Met Ser Ile Gly Gly

290 295 300

tta cca ggg aaa tta tca gac tgt tct gag caa gat gct aca aaa tgc 960

Leu Pro Gly Lys Leu Ser Asp Cys Ser Glu Gln Asp Ala Thr Lys Cys

305 310 315 320

gaa gta ttc ctt gta gag gga gat tcg gcg ggt ggt act gct aaa caa 1008

Glu Val Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Thr Ala Lys Gln

325 330 335

ggt agg gac aga aac ttt cag gca ata tta ccg ctt cgt ggt aaa atc 1056

Gly Arg Asp Arg Asn Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile

340 345 350

tta aat gtt gaa aaa gca atg caa cat aag gtt ttt gaa aac gaa gaa 1104
Leu Asn Val Glu Lys Ala Met Gln His Lys Val Phe Glu Asn Glu Glu
355 360 365

ata aaa aat att tac aca gct tta ggt gtt act att ggt aca gaa gaa 1152
Ile Lys Asn Ile Tyr Thr Ala Leu Gly Val Thr Ile Gly Thr Glu Glu
370 375 380

gat agt aaa gcc tta aac tta gaa aaa tta aga tac cat aaa gta gtt 1200
Asp Ser Lys Ala Leu Asn Leu Glu Lys Leu Arg Tyr His Lys Val Val
385 390 395 400

att atg tgt gat gcc gat gta gat ggt agc cac att gaa act tta atc 1248
Ile Met Cys Asp Ala Asp Val Asp Gly Ser His Ile Glu Thr Leu Ile
405 410 415

ctt aca ttc ttc ttc cgt ttt atg agg gag tta ata gaa ggc ggt cac 1296
Leu Thr Phe Phe Phe Arg Phe Met Arg Glu Leu Ile Glu Gly Gly His
420 425 430

gtt tat ata gca acc cca cct tta tac ttg gta aaa aag gga aca aaa 1344
Val Tyr Ile Ala Thr Pro Pro Leu Tyr Leu Val Lys Lys Gly Thr Lys
435 440 445

aaa cgt tat gct tgg aat gat aaa gaa cga gat gag ata gca gaa agc 1392
Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser
450 455 460

ttt aat ggt agt gtt ggt ata caa aga tat 1422
Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr
465 470

<210> 24

<211> 474

<212> PRT

<213> Cytophaga lytica

<400> 24

Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val
1 5 10 15

Ser Cys Val Asn Ala Leu Ser Asn Asn Leu Lys Ala Thr Val Tyr Arg
20 25 30

Glu Gly Lys Ile Trp Glu Gln Glu Tyr Glu Arg Gly Lys Ala Leu Tyr
35 40 45

Pro Val Lys Ser Ile Gly Glu Thr Glu Glu Thr Gly Thr Ile Val Thr
50 55 60

Phe Tyr Pro Asp Asp Thr Ile Phe Thr Gln Thr Thr Glu Tyr Asn Tyr
65 70 75 80

Glu Thr Leu Ser Asn Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly
85 90 95

Val Thr Ile Ser Ile Thr Asp Lys Arg Val Lys Asp Glu Lys Gly Glu
100 105 110

Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile
115 120 125

Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser
130 135 140

Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr
145 150 155 160

Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn
165 170 175

Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr
180 185 190

Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu
195 200 205

Lys Phe Glu Ile Gln Gly Asp Asp Phe Arg Glu Gly Leu Thr Ala Ile

210 215 220

Val Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr

225 230 235 240

Lys Leu Gly Asn Arg Glu Val Ser Ser Ala Val Ser Gln Ala Val Ser

245 250 255

Glu Met Leu Thr Asn Tyr Leu Glu Glu Asn Pro Asp Asp Ala Lys Val

260 265 270

Ile Val Gln Lys Val Ile Leu Ala Ala Gln Ala Arg His Ala Ala Thr

275 280 285

Lys Ala Arg Glu Met Val Gln Arg Lys Thr Val Met Ser Ile Gly Gly

290 295 300

Leu Pro Gly Lys Leu Ser Asp Cys Ser Glu Gln Asp Ala Thr Lys Cys

305 310 315 320

Glu Val Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Thr Ala Lys Gln

325 330 335

Gly Arg Asp Arg Asn Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile

340 345 350

Leu Asn Val Glu Lys Ala Met Gln His Lys Val Phe Glu Asn Glu Glu

355 360 365

Ile Lys Asn Ile Tyr Thr Ala Leu Gly Val Thr Ile Gly Thr Glu Glu

370 375 380

Asp Ser Lys Ala Leu Asn Leu Glu Lys Leu Arg Tyr His Lys Val Val

385 390 395 400

Ile Met Cys Asp Ala Asp Val Asp Gly Ser His Ile Glu Thr Leu Ile

405 410 415

Leu Thr Phe Phe Phe Arg Phe Met Arg Glu Leu Ile Glu Gly Gly His

420 425 430

Val Tyr Ile Ala Thr Pro Pro Leu Tyr Leu Val Lys Lys Gly Thr Lys

435 440 445

Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser
450 455 460

Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr
465 470

<210> 25

<211> 38

<212> PRT

<213> Artificial Sequence

<400> 25

tgtaaaacga cggccagtca ygcnggnggn aarttyga

<210> 26

<211> 7

<212> DNA

<213> Artificial Sequence

<400> 26

His Ala Gly Gly Lys Phe Asp
1 5

<210> 27

<211> 36

<212> DNA

<213> Artificial Sequence

<400> 27

ctgcgttcgt atatgagcnc crtcnacrtc ngcrtc 36

<210> 28

<211> 12

<212> PRT

<213> Artificial Sequence

<400> 28

Asp Ala Asp Val Asp Gly Ala His Ile Arg Thr Leu

1 5 10

<210> 29

<211> 41

<212> DNA

<213> Artificial Sequence

<400> 29

gaagtcatca tgaccgttct gcaygsnggn ggnaarttyg g 41

<210> 30

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 30

Glu Val Leu Met Thr Val Leu His Ala Gly Gly Lys Phe Gly

1 5 10

<210> 31

<210> 44

<211> DNA

<213> Artificial Sequence

<400> 31

agcagggtac ggatgtgcga gccrtcnacr tcngcrtcng tgat 44

<210> 32

<211> 15

<212> PRT

<213> Artificial Sequence

<400> 32

Met Thr Asp Ala Asp Val Asp Gly Ser His Ile Arg Thr Leu Leu

1 5 10 15

<210> 33

<211> 32

<212> DNA

<213> Artificial Sequence

<400> 33

caggaaacag ctatgaccar rtgngtnccn cc 32

<210> 34

<211> 5

<212> PRT

<213> Artificial Sequence

<400> 34

Gly Gly Thr His Leu

1 5

<210> 35

<211> 34

<212> DNA

<213> Artificial Sequence

<400> 35

gcaacgagat caacactcmn garggnggna cnca 34

<210> 36

<211> 11

<212> PRT

<213> Artificial Sequence

<400> 36

Asn Asn Ile Asn Thr His Glu Gly Gly Thr His

1 5 10

<210> 37

<211> 11

<212> PRT

<213> Artificial Sequence

<400> 37

Asn Asn Ile Asn Thr Pro Glu Gly Gly Thr His

1 5 10

<210> 38

<211> 35

<212> DNA

<213> Artificial Sequence

<400> 38

tgtaaaacga cggccagtar yttnkyyttn gtytg 35

<210> 39

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 39

Gln Thr Lys Thr Lys Leu

1 5

<210> 40

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 40

Gln Thr Lys Asp Lys Leu

1 5

<210> 41

<211> 35

<212> DNA

<213> Artificial Sequence

<400> 41

taggctagct gaccgtaaga ygcngayrtn gaygg 35

<210> 42

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 42

Asp Ala Asp Val Asp Gly

1 5

<210> 43

<211> 36

<212> DNA

<213> Artificial Sequence

<400> 43

ccatagctgc gtagcattca tytcnccnar nccytt 36

<210> 44

<211> 12

<212> PRT

<213> Artificial Sequence

<400> 44

Lys Gly Leu Gly Glu Met Asn Ala Thr Gln Leu Trp

1 5 10

<210> 45

<211> 41

<212> DNA

<213> Artificial Sequence

<400> 45

caggaaacag ctatgaccaa rmgnccngsn atgtayathg g 41

<210> 46

<211> 8

<212> PRT

<213> Artificial Sequence

<400> 46

Lys Arg Pro Ala Met Tyr Ile Gly

1 5

<210> 47

<211> 8

<212> PRT

<213> Artificial Sequence

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Lys Arg Pro Gly Met Tyr Ile Gly

1 5

<210> 48

<211> 38

<212> DNA

<213> Artificial Sequence

<400> 48

tgtaaaacga cggccagtcc nccngcnswr tcnccytc 38

<210> 49

<211> 7

<212> PRT

<213> Artificial Sequence

<400> 49

Glu Gly Asp Ser Ala Gly Gly

1 5

<210> 50

<211> 39

<212> DNA

<213> Artificial Sequence

<400> 50

tgtaaaacga cggccagtca tngtngtntc ccanarytg 39

<210> 51

<211> 7

<212> PRT

<213> Artificial Sequence

<400> 51

Gln Leu Trp Glu Thr Thr Met

1 5

<210> 52

<211> 7

<212> PRT

<213> Artificial Sequence

<400> 52

Gln Leu Trp Asp Thr Thr Met

1 5

<210> 53

<211> 41

<212> DNA

<213> Artificial Sequence

<400> 53

gaagtcatca tgaccgttct gcaygcnggn ggnaarttyg a 41

<210> 54

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 54

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asp

1 5 10

<210> 55

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 55

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asn

1 5 10

<210> 56

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 56

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Glu

1 5 10

<210> 57

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 57

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Lys

1 5 10

<210> 58

<211> 38

<212> DNA

<213> Artificial Sequence

<400> 58

tgtaaaacga cggccagtgc nggrtcytty tcytgrca 38

<210> 59

<211> 7

<212> PRT

<213> Artificial Sequence

<400> 59

Cys Gln Glu Lys Asp Pro Ala

1 5

<210> 60

<211> 40

<212> DNA

<213> Artificial Sequence

<400> 60

gaagtcatca tgaccgttct gcaacnaaya ayathccnca 40

<210> 61

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 61

Thr Asn Asn Ile Pro Gln

1 5

<210> 62

<211> 38

<212> DNA

<213> Artificial Sequence

<400> 62

tgtaaaacga cggccagtaa yttnggntcn ggnacytt 38

<210> 63

<211> 7

<212> PRT

<213> Artificial Sequence

<400> 63

Lys Val Pro Asp Pro Lys Phe

1 5

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<400> 64

Lys Val Pro Glu Pro Lys Phe

1 5

<210> 65

<211> 35

<212> DNA

<213> Artificial Sequence

<400> 65

caggaaacag ctatgaccgc nmrnmrngcn mgnga 35

<210> 66

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 66

Ala Arg Arg Ala Arg Glu

1 5

<210> 67

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 67

Ala Arg Lys Ala Arg Glu

1 5

<210> 68

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 68

Ala Lys Lys Ala Arg Glu

1 5

<210> 69

<211> 19

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Pro or Ser; Xaa2 = Ala or Thr; Xaa3 = Ala, Val or Leu; Xaa4 = Glu or Asp; Xaa5 = Val or Thr; Xaa6 = Ile or Val; Xaa7 = Met, Leu or Phe; Xaa8 = Val, Gln or Ile; Xaa9 = Asp or Gly; Xaa10 = Asp, Gly, Asn or Ser; Xaa11 = Ser, Lys, Gly, Asp or Asn

<400> 69

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Leu His Ala Gly Gly Lys Phe

1 5 10 15

Xaa Xaa Xaa

<210> 70

<211> 4

<212> PRT

<213> Artificial Sequence

<400> 70

Gly Gly Thr His

1

<210> 71

<211> 15

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Ile or Leu; Xaa2 = Ala or Ser

<400> 71

Xaa Met Thr Asp Ala Asp Val Asp Gly Xaa His Ile Arg Thr Leu

1 5 10 15

<210> 72

<211> 11

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Gly or Ala; Xaa2 = Ser or Asp

<400> 72

Arg Lys Arg Pro Xaa Met Tyr Ile Gly Xaa Thr

1 5 10

<210> 73

<211> 6

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Thr or Pro; Xaa2 = Lys or Asn; Xaa3 = Thr, Asp, Gly, Lys, Ser, Phe or Tyr

<400> 73

Gln Xaa Xaa Xaa Lys Leu

1 5

<210> 74

<211> 9

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Tyr or Phe; Xaa2 = Ala or Pro

<400> 74

Xaa Lys Gly Leu Gly Glu Met Asn Xaa

1 5

<210> 75

<211> 9

<212> PRT

<213> Artificial Sequence

<400> 75

Val Glu Gly Asp Ser Ala Gly Gly Ser

1 5

<210> 76

<211> 7

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = His or Val; Xaa2 = Gln or Lys

<400> 76

Lys Xaa Pro Asp Pro Xaa Phe

1 5

<210> 77

<211> 14

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Ser or Gln; Xaa2 = Ser or Glu; Xaa3 = Lys or Arg; Xaa4 = Ala or Ser

<400> 77

Leu Pro Gly Lys Leu Ala Asp Cys Xaa Xaa Xaa Asp Pro Xaa

1 5 10

<210> 78

<211> 9

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Trp or Arg; Xaa2 = Glu or Asp; Xaa3 = Met or Leu; Xaa4 = Asp or Asn

<400> 78

Gln Leu Xaa Xaa Thr Thr Xaa Xaa Pro

1 5

<210> 79

<211> 6

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Lys or Arg; Xaa2 = Lys or Arg

<400> 79

Ala Xaa Xaa Ala Arg Glu

1 5

<210> 80

<211> 7

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Pro or Asn; Xaa2 = Thr or Gln

<400> 80

Phe Thr Asn Asn Ile Xaa Xaa

1 5